SEQUENCE LISTING

```
<110> WILKINS, TRACEY D.
   LYERLY, DAVID M.
   MONCRIEF, J. SCOTT
   PAVLIAKOVA, DANKA
   SCHNEERSON, RACHEL
   ROBBINS, JOHN B.
```

<130> 420522000100

<140> 09/545,772

<141> 2000-04-14

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 2507

<212> DNA

<213> Clostridium difficile

<400> 1

```
gatcctatag aatttaactt agtaactgga tggcaaacta tcaatggtaa aaaatattat 60
tttgatataa atactggagc agctttaact agttataaaa ttattaatgg taaacacttt 120
tattttaata atgatggtgt gatgcagttg ggagtattta aaggacctga tggatttgaa 180
tattttgcac ctgccaatac tcaaaataat aacatagaag gtcaggctat agtttatcaa 240
agtaaattct taactttgaa tggcaaaaaa tattattttg ataataactc aaaagcagtc 300
actggatgga gaattattaa caatgagaaa tattacttta atcctaataa tgctattgct 360
gcagtcggat tgcaagtaat tgacaataat aagtattatt tcaatcctga cactgctatc 420
atctcaaaag gttggcagac tgttaatggt agtagatact actttgatac tgataccgct 480
attgccttta atggttataa aactattgat ggtaaacact tttattttga tagtgattgt 540
gtagtgaaaa taggtgtgtt tagtacctct aatggatttg aatattttgc acctgctaat 600
acttataata ataacataga aggtcaggct atagtttatc aaagtaaatt cttaactttg 660
aatggtaaaa aatattactt tgataataac tcaaaagcag ttaccggatg gcaaactatt 720
gatagtaaaa aatattactt taatactaac actgctgaag cagctactgg atggcaaact 780
attgatggta aaaaatatta ctttaatact aacactgctg aagcagctac tggatggcaa 840
actattgatg gtaaaaaata ttactttaat actaacactg ctatagcttc aactggttat 900
acaattatta atggtaaaca tttttatttt aatactgatg gtattatgca gataggagtg 960
tttaaaggac ctaatggatt tgaatatttt gcacctgcta atacggatgc taacaacata 1020
gaaggtcaag ctatacttta ccaaaatgaa ttcttaactt tgaatggtaa aaaatattac 1080
tttggtagtg actcaaaagc agttactgga tggagaatta ttaacaataa gaaatattac 1140
tttaatccta ataatgctat tgctgcaatt catctatgca ctataaataa tgacaagtat 1200
tactttagtt atgatggaat tcttcaaaat ggatatatta ctattgaaag aaataatttc 1260
tattttgatg ctaataatga atctaaaatg gtaacaggag tatttaaagg acctaatgga 1320
tttgagtatt ttgcacctgc taatactcac aataataaca tagaaggtca ggctatagtt 1380
taccagaaca aattettaac tttgaatggc aaaaaatatt attttgataa tgactcaaaa 1440
gcagttactg gatggcaaac cattgatggt aaaaaatatt actttaatct taacactgct 1500
gaagcagcta ctggatggca aactattgat ggtaaaaaat attactttaa tcttaacact 1560
gctgaagcag ctactggatg gcaaactatt gatggtaaaa aatattactt taatactaac 1620
actttcatag cctcaactgg ttatacaagt attaatggta aacattttta ttttaatact 1680
gatggtatta tgcagatagg agtgtttaaa ggacctaatg gatttgaata ctttgcacct 1740
gctaatacgg atgctaacaa catagaaggt caagctatac tttaccaaaa taaattctta 1800
actttgaatg gtaaaaaata ttactttggt agtgactcaa aagcagttac cggactgcga 1860
```

actattgatg	gtaaaaaata	ttactttaat	actaacactg	ctgttgcagt	tactggatgg	1920
caaactatta	atggtaaaaa	atactacttt	aatactaaca	cttctatagc	ttcaactggt	1980
					gcagatagga	
gtgtttaaag	gacctgatgg	atttgaatac	tttgcacctg	ctaatacaga	tgctaacaat	2100
					caatatatat	
					taatagatat	
tacttcgagc	ctaatacagc	tatgggtgcg	aatggttata	aaactattga	taataaaaat	2280
ttttacttta	gaaatggttt	acctcagata	ggagtgttta	aagggtctaa	tggatttgaa	2340
					acgttatcaa	
aatagattcc	tacatttact	tggaaaaata	tattactttg	gtaataattc	aaaagcagtt	2460
actggatggc	aaactattaa	tggtaaagta	tattacttta	tgcctga		2507

<210> 2

<211> 866

<212> PRT

<213> Clostridium difficile

<400> 2

Asp Pro Ile Glu Phe Asn Leu Val Thr Gly Trp Gln Thr Ile Asn Gly
1 5 10 15

Lys Lys Tyr Tyr Phe Asp Ile Asn Thr Gly Ala Ala Leu Thr Ser Tyr 20 25 30

Lys Ile Ile Asn Gly Lys His Phe Tyr Phe Asn Asn Asp Gly Val Met 35 40 45

Gln Leu Gly Val Phe Lys Gly Pro Asp Gly Phe Glu Tyr Phe Ala Pro 50 55 60

Ala Asn Thr Gln Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr Gln 65 70 75 80

Ser Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn Asn 85 90 95

Ser Lys Ala Val Thr Gly Trp Arg Ile Ile Asn Asn Glu Lys Tyr Tyr 100 105 110

Phe Asn Pro Asn Asn Ala Ile Ala Ala Val Gly Leu Gln Val Ile Asp 115 120 125

Asn Asn Lys Tyr Tyr Phe Asn Pro Asp Thr Ala Ile Ile Ser Lys Gly
130 140

Trp Gln Thr Val Asn Gly Ser Arg Tyr Tyr Phe Asp Thr Asp Thr Ala 145 150 155 160

Ile Ala Phe Asn Gly Tyr Lys Thr Ile Asp Gly Lys His Phe Tyr Phe 165 170 175

Asp Ser Asp Cys Val Val Lys Ile Gly Val Phe Ser Thr Ser Asn Gly
180 185 190

Phe Glu Tyr Phe Ala Pro Ala Asn Thr Tyr Asn Asn Ile Glu Gly 195 200 205 Gln Ala Ile Val Tyr Gln Ser Lys Phe Leu Thr Leu Asn Gly Lys Lys 215 Tyr Tyr Phe Asp Asn Asn Ser Lys Ala Val Thr Gly Trp Gln Thr Ile 235 230 Asp Ser Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Glu Ala Ala Thr 250 Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr 265 Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr 280 Phe Asn Thr Asn Thr Ala Ile Ala Ser Thr Gly Tyr Thr Ile Ile Asn 290 295 Gly Lys His Phe Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val 310 Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Leu Tyr Gln Asn Glu Phe Leu 345 Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Trp Arg Ile Ile Asn Asn Lys Lys Tyr Tyr Phe Asn Pro Asn 375 Asn Ala Ile Ala Ile His Leu Cys Thr Ile Asn Asn Asp Lys Tyr Tyr Phe Ser Tyr Asp Gly Ile Leu Gln Asn Gly Tyr Ile Thr Ile Glu 410 Arg Asn Asn Phe Tyr Phe Asp Ala Asn Asn Glu Ser Lys Met Val Thr Gly Val Phe Lys Gly Pro Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr His Asn Asn Asn Ile Glu Gly Gln Ala Ile Val Tyr Gln Asn Lys 450 Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Asp Asn Asp Ser Lys 475 Ala Val Thr Gly Trp Gln Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln Thr Ile Asp Gly Lys 500 505

Lys Tyr Tyr Phe Asn Leu Asn Thr Ala Glu Ala Ala Thr Gly Trp Gln 520 Thr Ile Asp Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Phe Ile Ala 535 Ser Thr Gly Tyr Thr Ser Ile Asn Gly Lys His Phe Tyr Phe Asn Thr 555 Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asn Gly Phe Glu 570 Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln Ala Ile Leu Tyr Gln Asn Lys Phe Leu Thr Leu Asn Gly Lys Lys Tyr Tyr Phe Gly Ser Asp Ser Lys Ala Val Thr Gly Leu Arg Thr Ile Asp Gly 615 Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ala Val Ala Val Thr Gly Trp 630 Gln Thr Ile Asn Gly Lys Lys Tyr Tyr Phe Asn Thr Asn Thr Ser Ile 650 645 Ala Ser Thr Gly Tyr Thr Ile Ile Ser Gly Lys His Phe Tyr Phe Asn Thr Asp Gly Ile Met Gln Ile Gly Val Phe Lys Gly Pro Asp Gly Phe 680 Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gly Gln 695 Ala Ile Arg Tyr Gln Asn Arg Phe Leu Tyr Leu His Asp Asn Ile Tyr 715 Tyr Phe Gly Asn Asn Ser Lys Ala Ala Thr Gly Trp Val Thr Ile Asp Gly Asn Arg Tyr Tyr Phe Glu Pro Asn Thr Ala Met Gly Ala Asn Gly Tyr Lys Thr Ile Asp Asn Lys Asn Phe Tyr Phe Arg Asn Gly Leu Pro Gln Ile Gly Val Phe Lys Gly Ser Asn Gly Phe Glu Tyr Phe Ala Pro Ala Asn Thr Asp Ala Asn Asn Ile Glu Gln Ala Ile Arg Tyr Gln Asn 790 Arg Phe Leu His Leu Leu Gly Lys Ile Tyr Tyr Phe Gly Asn Asn Ser 810 805

Lys Ala Val Thr Gly Gly Trp Gln Thr Ile Asn Gly Lys Val Tyr Tyr 820 825 830

Phe Met Pro Asp Thr Ala Met Ala Ala Ala Gly Gly Leu Phe Glu Asp 835 840 845

Gly Val Ile Tyr Phe Phe Gly Val Asp Gly Val Lys Ala Pro Gly Ile 850 855 860

Tyr Gly 865